



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

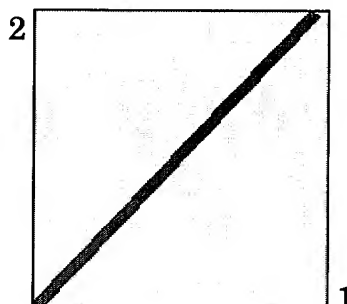
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒

Sequence gi Homo sapiens solute carrier family 25  
 1 21361113 (mitochondrial carrier; oxoglutarate carrier), Length 1570 (1 .. 1570)  
 member 11 (SLC25A11), mRNA

Sequence gi  
 2 3387910 Length 1503 (1 .. 1503)



Seq Alignment

of 2136113 (seq1)  
 & 3387910 (seq2)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2832 bits (1473), Expect = 0.0  
 Identities = 1475/1476 (99%)  
 Strand = Plus / Plus

```

Query:                22  ggcggtgcgcgcgccctcgctctgttgcgcgcgcggtgtcaccttgggc
                        |||
Sbjct:                11  ggcggtgcgcgcgccctcgctctgttgcgcgcgcggtgtcaccttgggc

Query:                82  gcgcgcgcacgggacccggagccgagggccattgagtggcgatggcgg
                        | |||
Sbjct:                71  gtgcgcgcacgggacccggagccgagggccattgagtggcgatggcgg
2-oxoglutarate carrier protein 1                               M  A

Query:               142  ccggggccggcgggatagacgggaagccccgtacctcccctaagtccg
                        |||
Sbjct:               131  ccggggccggcgggatagacgggaagccccgtacctcccctaagtccg
2-oxoglutarate carrier protein 7  A G A G G I D G K P R T S P K S
  
```

Query: 802 tgatcagcgggtcttgtcaccactgctgcctccatgcctgtggacattg  
|||||  
Sbjct: 791 tgatcagcgggtcttgtcaccactgctgcctccatgcctgtggacattg  
2-oxoglutarate carrier protein 227 M I S G L V T T A A S M P V D I

Query: 862 tccagaacatgcggatgattgatgggaagccggaatacaagaacgggc  
|||||  
Sbjct: 851 tccagaacatgcggatgattgatgggaagccggaatacaagaacgggc  
2-oxoglutarate carrier protein 247 I Q N M R M I D G K P E Y K N G

Query: 922 tcaaagttgtccgctacgagggttcttcagcctgtggaagggttca  
|||||  
Sbjct: 911 tcaaagttgtccgctacgagggttcttcagcctgtggaagggttca  
2-oxoglutarate carrier protein 267 F K V V R Y E G F F S L W K G F

Query: 982 cccgcctgggccccacaccgtcctcaccttcatcttcttggagcaga  
|||||  
Sbjct: 971 cccgcctgggccccacaccgtcctcaccttcatcttcttggagcaga  
2-oxoglutarate carrier protein 287 A R L G P H T V L T F I F L E Q

Query: 1042 acaagcgtctcttctcctcagtggtgaagcggccgggggtcccactcg  
|||||  
Sbjct: 1031 acaagcgtctcttctcctcagtggtgaagcggccgggggtcccactcg  
2-oxoglutarate carrier protein 307 Y K R L F L S G ^^^

Query: 1102 atagccactgcgccctgggggcctgggctctgctgccctggaccctc  
|||||  
Sbjct: 1091 atagccactgcgccctgggggcctgggctctgctgccctggaccctc

Query: 1162 ttccacagtgtggtttcttctctgcggtaaaggacttggtctgttct  
|||||  
Sbjct: 1151 ttccacagtgtggtttcttctctgcggtaaaggacttggtctgttct

Query: 1222 agcttgccctgctcgtcctgatcctgtgatttctctgtccttggctat  
|||||  
Sbjct: 1211 agcttgccctgctcgtcctgatcctgtgatttctctgtccttggctat

Query: 1282 ctggaaaacttctgaggatttctggcctccccctgggttttagtttc  
|||||  
Sbjct: 1271 ctggaaaacttctgaggatttctggcctccccctgggttttagtttc

Query: 1342 acagcagaagatccccttggcagtggggaaaccaaggcagagctgag  
|||||  
Sbjct: 1331 acagcagaagatccccttggcagtggggaaaccaaggcagagctgag

Query: 1402 agcagaagccatcaagatggtcaaaggcctgcagaggagatgtggc  
|||||  
Sbjct: 1391 agcagaagccatcaagatggtcaaaggcctgcagaggagatgtggc

Query: 1462 tcattgaggacttaataaattggattgatgacacca 1497  
|||||  
Sbjct: 1451 tcattgaggacttaataaattggattgatgacacca 1486

CPU time: 0.08 user secs. 0.03 sys. secs 0.11 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 8  
Number of Sequences: 0  
Number of extensions: 8  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
length of query: 1570  
length of database: 7,833,321,048  
effective HSP length: 25  
effective length of query: 1545  
effective length of database: 7,833,321,023  
effective search space: 12102480980535  
effective search space used: 12102480980535  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)



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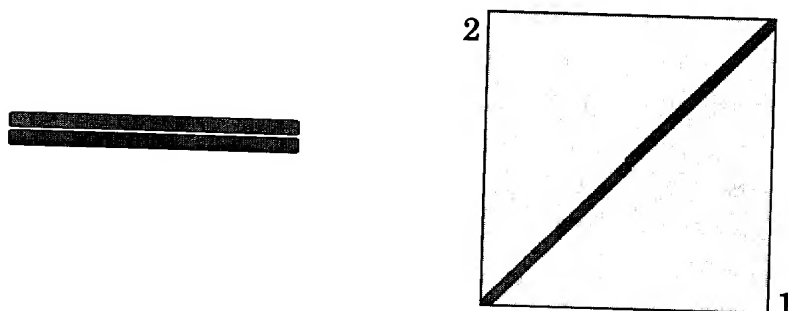
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.00** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq\_1 Length 314 (1 .. 314)

Sequence 2 lcl|seq\_2 Length 314 (1 .. 314)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 622 bits (1603), Expect = e-177  
 Identities = 314/314 (100%), Positives = 314/314 (100%)

```

Query: 1  MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
          MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE
Sbjct: 1  MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60

Query: 61 YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFRLTGADGTPPGFL 120
          YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFRLTGADGTPPGFL
Sbjct: 61 YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFRLTGADGTPPGFL 120

Query: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLT 180
          LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLT
Sbjct: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLT 180

Query: 181 WRGCIPTMARAVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV 240
          WRGCIPTMARAVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV
Sbjct: 181 WRGCIPTMARAVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV 240

Query: 241 DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL 300
          DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL
Sbjct: 241 DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL 300

Query: 301 EQMNKAYKRLFLSG 314
          EQMNKAYKRLFLSG
Sbjct: 301 EQMNKAYKRLFLSG 314
  
```

Alignment of aa encoded by NM-003562 (seq1)  
 and A070548 (seq2)

100% match

CPU time: 0.09 user secs. 0.02 sys. secs 0.11 total secs.

Lambda	K	H
0.323	0.138	0.404

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1236

Number of Sequences: 0

Number of extensions: 82

Number of successful extensions: 9

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 314

length of database: 422,818,587

effective HSP length: 126

effective length of query: 188

effective length of database: 422,818,461

effective search space: 79489870668

effective search space used: 79489870668

T: 9

A: 40

X1: 16 ( 7.5 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (22.0 bits)

S2: 74 (33.1 bits)